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Supplementary Data

Identification of Novel Candidate Genes for Alzheimer's Disease by Autozygosity Mapping using Genome Wide SNP Data

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Supplementary Table S1
SNPs in homozygous regions associated with AD in Wadi Ara at $p \leq 0.05$

Chr	SNP	Position	MAF case	MAF control	OR	p	Quality	Gene	Type
2	rs1872788	62671182	0.35	0.44	0.60	0.04	0.88	NA	NA
2	rs901530	62671771	0.35	0.44	0.60	0.04	0.88	NA	NA
2	rs6753844	62673907	0.35	0.44	0.60	0.04	0.88	NA	NA
2	rs4671432	62676846	0.34	0.43	0.61	0.04	0.89	NA	NA
2	rs1014119	62678986	0.33	0.43	0.61	0.04	0.90	NA	NA
6	rs537160	32024379	0.12	0.06	2.37	0.03	0.98	CFB	intron
6	rs12333245	32127747	0.19	0.26	0.59	0.02	1.00	TNXB	intron
6	rs1009382	32134085	0.25	0.18	1.77	0.03	0.94	TNXB	missense
6	rs2269429	32137161	0.19	0.26	0.59	0.02	1.00	TNXB	missense
6	rs9469079	32140399	0.18	0.25	0.58	0.02	0.99	TNXB	intron
6	rs9469080	32143405	0.19	0.26	0.60	0.03	1.00	TNXB	intron
6	rs3749962	32144335	0.19	0.26	0.60	0.03	1.00	TNXB	synonymous
6	rs9469082	32148909	0.19	0.26	0.60	0.03	1.00	TNXB	intron
6	rs3130286	32150300	0.17	0.12	1.87	0.05	0.95	TNXB	intron
6	rs204877	32155414	0.19	0.26	0.61	0.03	1.00	TNXB	intron
6	rs169496	32160961	0.19	0.26	0.61	0.03	1.00	TNXB	intron
6	rs3134950	32235455	0.34	0.26	1.63	0.03	0.92	PPT2	intron
6	rs1061808	32244525	0.33	0.26	1.66	0.02	0.91	AGPAT1	3′UTR
6	rs3130283*	32246523	0.11	0.06	3.13	0.004	0.96	AGPAT1	intron
6	rs2269423	32253685	0.32	0.24	1.67	0.02	0.96	AGPAT1	intron
6	rs3134943	32255739	0.10	0.04	3.66	0.002	1.00	RNF5	intron
6	rs1800684	32259972	0.09	0.03	4.36	0.002	0.98	AGER	synonymous
6	rs1044506	32280043	0.08	0.04	3.73	0.03	0.96	NOTCH4	synonymous
6	rs3131294	32288124	0.10	0.05	2.82	0.04	0.93	NOTCH4	intron
6	rs396960	32299559	0.28	0.36	0.61	0.03	0.92	NOTCH4	intron
8	rs13271711	49526732	0.04	0.07	0.24	0.04	0.92	NA	NA
8	rs10089053	49660586	0.08	0.06	3.25	0.05	0.89	NA	NA
8	rs4424286	49671053	0.08	0.06	3.86	0.03	0.90	NA	NA
9	rs10868248	71703997	0.12	0.07	2.66	0.01	0.99	C9orf135	intron
9	rs7863165	71764547	0.18	0.11	2.07	0.01	0.98	NA	NA
9	rs10735572	71765581	0.06	0.04	3.32	0.03	0.95	NA	NA
9	rs7037671	71766818	0.06	0.04	3.32	0.03	0.95	NA	NA
9	rs4574911	71797023	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs1027284	71799485	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs10868358	71801500	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs4744583	71801754	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs870011	71804632	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs953372	71805689	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs4418399	71806161	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs4403478	71806885	0.17	0.11	2.33	0.007	0.98	NA	NA
9	rs7035415	71808349	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs7863229	71808783	0.17	0.10	2.42	0.005	1.00	NA	NA
9	rs7859880	71843256	0.20	0.27	0.55	0.02	0.90	NA	NA
9	rs755778	71850379	0.19	0.26	0.59	0.03	0.93	MAMDC2	intron
9	rs2997657	71852509	0.19	0.26	0.59	0.03	0.93	MAMDC2	intron
9	rs12352964	71856948	0.09	0.14	0.41	0.01	0.92	MAMDC2	intron
9	rs3015237	71859460	0.13	0.20	0.57	0.02	1.00	MAMDC2	intron
9	rs4744970	71861470	0.13	0.20	0.57	0.02	1.00	MAMDC2	intron
9	rs4744972	71861846	0.13	0.20	0.57	0.02	1.00	MAMDC2	intron
9	rs3015239	71862722	0.11	0.16	0.51	0.02	0.96	MAMDC2	intron
9	rs7035878	71875979	0.13	0.20	0.57	0.02	1.00	MAMDC2	intron
9	rs11141566	71885934	0.14	0.20	0.61	0.04	1.00	MAMDC2	intron
9	rs4237238	71900383	0.14	0.20	0.61	0.04	1.00	MAMDC2	intron
9	rs12341763	71900928	0.11	0.17	0.52	0.01	1.00	MAMDC2	intron
9	rs4237239	71903716	0.14	0.21	0.61	0.03	0.99	MAMDC2	intron
9	rs6559970	71917562	0.15	0.21	0.61	0.03	1.00	MAMDC2	intron
9	rs1927107	71918553	0.15	0.21	0.61	0.03	1.00	MAMDC2	intron
9	rs4744979	71922475	0.15	0.21	0.60	0.03	1.00	MAMDC2	intron
9	rs7853094	71925881	0.15	0.21	0.60	0.03	1.00	MAMDC2	intron
9	rs12349576	71927401	0.15	0.21	0.60	0.03	1.00	MAMDC2	intron
9	rs4744983	71949873	0.11	0.17	0.52	0.01	0.99	MAMDC2	intron

Supplementary Table S1
Continued

Chr	SNP	Position	MAF case	MAF control	OR	*p*	Quality	Gene	Type
9	rs10868610	71954693	0.11	0.17	0.52	0.01	0.99	MAMDC2	intron
9	rs11794396	71992354	0.11	0.17	0.52	0.01	0.99	MAMDC2	intron
9	rs11142019	71992659	0.11	0.17	0.52	0.01	0.99	MAMDC2	intron
9	rs2148856	72001259	0.11	0.17	0.52	0.01	0.99	MAMDC2	intron
9	rs11142141	72020229	0.11	0.17	0.52	0.01	0.99	MAMDC2	intron
9	rs7873075	72034009	0.11	0.17	0.52	0.01	0.99	NA	NA
9	rs1180085	72057147	0.11	0.17	0.52	0.01	0.99	NA	NA
9	rs1180109	72075087	0.10	0.17	0.53	0.01	1.00	SMC5	intron
9	rs1180116	72087254	0.11	0.17	0.54	0.02	1.00	SMC5	missense
9	rs10868798	72092323	0.11	0.17	0.54	0.02	0.99	SMC5	intron
9	rs1180131	72095224	0.11	0.17	0.54	0.02	1.00	SMC5	intron
9	rs11142355	72100553	0.11	0.17	0.54	0.02	1.00	SMC5	intron
9	rs7849942	72122702	0.11	0.16	0.55	0.03	0.99	SMC5	intron
9	rs12346675	72147361	0.11	0.17	0.56	0.02	0.99	SMC5	intron
9	rs7847861	72162634	0.11	0.16	0.58	0.03	1.00	NA	NA
9	rs12684881	72167165	0.11	0.16	0.59	0.03	1.00	NA	NA
9	rs4745006	72175706	0.15	0.20	0.56	0.04	0.90	NA	NA
9	rs7875663	72289023	0.44	0.33	1.77	0.005	0.97	NA	NA
9	rs7849735	72289274	0.48	0.38	1.55	0.02	0.99	NA	NA
9	rs6560138	72289908	0.48	0.38	1.55	0.02	0.99	NA	NA
9	rs3923700	72292598	0.48	0.38	1.56	0.02	1.00	NA	NA
9	rs3923699	72292644	0.44	0.33	1.77	0.00	0.97	NA	NA
9	rs3901151	72292961	0.48	0.38	1.56	0.02	1.00	NA	NA
9	rs7018675	72293046	0.48	0.38	1.56	0.02	1.00	NA	NA
9	rs10868838	72294131	0.25	0.18	1.53	0.04	0.97	NA	NA
9	rs4472581	72294703	0.48	0.38	1.56	0.02	0.98	NA	NA
9	rs10868839	72294896	0.25	0.18	1.53	0.04	0.97	NA	NA
9	rs6560139	72295317	0.48	0.38	1.56	0.02	0.98	NA	NA
9	rs7856642	72296173	0.49	0.38	1.56	0.02	0.98	NA	NA
9	rs11792173	72298171	0.49	0.38	1.54	0.03	0.97	NA	NA
9	rs9969768	72300708	0.50	0.39	1.54	0.03	0.98	NA	NA
9	rs7847938	72300995	0.50	0.39	1.54	0.03	0.98	NA	NA
9	rs7024178	72302374	0.26	0.18	1.53	0.04	0.98	NA	NA
9	rs7871523	72304099	0.50	0.39	1.53	0.03	0.98	NA	NA
9	rs10868840	72304518	0.26	0.18	1.53	0.04	0.98	NA	NA
9	rs10868841	72308484	0.26	0.18	1.53	0.04	0.98	NA	NA
9	rs10868843	72309535	0.50	0.39	1.53	0.03	0.98	NA	NA
9	rs7032346	72309852	0.50	0.39	1.53	0.03	0.98	NA	NA
9	rs10868845	72310966	0.26	0.18	1.56	0.04	0.97	NA	NA
9	rs7037072	72311118	0.50	0.39	1.53	0.03	0.98	NA	NA
9	rs10780936	72311143	0.26	0.18	1.57	0.04	0.96	NA	NA
9	rs4744600	72337348	0.30	0.22	1.62	0.02	0.93	NA	NA
9	rs10868854	72383191	0.42	0.33	1.50	0.03	1.00	TRPM3	intron
9	rs10780951	72383357	0.42	0.33	1.49	0.03	0.99	TRPM3	intron
9	rs11142509	72423141	0.20	0.14	1.83	0.05	0.93	TRPM3	intron
9	rs7027906	72471178	0.26	0.18	1.65	0.04	0.99	TRPM3	intron
9	rs11142539	72474803	0.26	0.18	1.65	0.04	1.00	TRPM3	intron
9	rs4131069	72475275	0.26	0.18	1.65	0.04	1.00	TRPM3	intron
9	rs4540466	72477527	0.25	0.18	1.66	0.04	0.99	TRPM3	intron
9	rs1011308	72478076	0.26	0.18	1.64	0.04	1.00	TRPM3	intron
9	rs7874138	72485540	0.26	0.18	1.63	0.04	1.00	TRPM3	intron
9	rs12378618	72496209	0.22	0.15	1.76	0.04	0.98	TRPM3	intron
9	rs12344255	72497811	0.24	0.17	1.66	0.05	0.97	TRPM3	intron
15	rs11638769	86659786	0.09	0.12	0.30	0.03	0.81	NA	NA
15	rs1256841	88349309	0.05	0.08	0.44	0.02	1.00	ZNF710	intron

*SNPs were nominally associated with AD in the meta-analysis, OR = odds ratio, Quality = the posterior probability of a correctly imputed genotype.

Supplementary Table S2
SNPs associated with AD at $p < 10^{-4}$ in Wadi Ara

Chr	SNP	BP	MAF case	MAF control	OR	p	Quality	Gene	SNP type
1	rs4457599	83885479	0.52	0.40	2.77	1.77E-05	0.87	NA	NA
1	rs4539154	83885747	0.52	0.40	2.77	1.76E-05	0.87	NA	NA
1	rs2068611	83886234	0.52	0.40	2.78	1.75E-05	0.87	NA	NA
1	rs4907035	83887487	0.29	0.47	0.25	2.74E-07	0.83	NA	NA
1	rs12127377	114291496	0.29	0.17	2.78	8.89E-05	0.95	HIPK1	intron
1	rs1553450	114292303	0.29	0.17	2.86	8.03E-05	0.94	HIPK1	intron
1	rs11102707	114295106	0.29	0.17	2.89	7.90E-05	0.93	HIPK1	intron
1	rs12129050	114298130	0.30	0.18	0.35	8.06E-05	0.92	HIPK1	intron
1	rs11102709	114313606	0.29	0.17	2.96	7.36E-05	0.92	HIPK1	intron
1	rs10108	114317853	0.29	0.17	2.86	7.23E-05	0.92	HIPK1	3′UTR
1	rs12032159	217653038	0.30	0.17	2.99	5.46E-05	0.96	NA	NA
1	rs2124328	217654860	0.30	0.17	2.99	5.07E-05	0.97	NA	NA
1	rs2791559	217655426	0.37	0.23	2.86	2.52E-05	0.99	NA	NA
2	rs741472	71290362	0.21	0.36	0.44	8.13E-05	1.00	PAIP2B	intron
2	rs2593708	134695885	0.40	0.55	0.39	2.79E-05	0.86	NA	NA
3	rs7621429	32277533	0.46	0.31	2.57	5.66E-05	0.89	CMTM8	intron
3	rs4245886	32279107	0.46	0.31	2.56	5.52E-05	0.89	CMTM8	intron
3	rs7636660	32287918	0.44	0.28	2.78	1.82E-05	0.90	CMTM8	intron
3	rs4572808	32292718	0.43	0.27	2.86	1.82E-05	0.88	CMTM8	intron
3	rs7644602	32295412	0.45	0.29	2.61	2.28E-05	0.94	CMTM8	intron
3	rs11708149	32296603	0.49	0.32	2.58	2.47E-05	0.92	CMTM8	intron
3	rs6783478	32297979	0.49	0.32	2.60	2.46E-05	0.91	CMTM8	intron
3	rs4955274	32302425	0.45	0.29	3.07	1.02E-05	0.84	CMTM8	intron
4	rs6853435	154925466	0.50	0.35	2.32	4.46E-05	0.95	SFRP2	intron
4	rs3810765	154928930	0.50	0.35	2.32	4.47E-05	0.95	SFRP2	intron
4	rs1456389	154933566	0.50	0.35	2.31	4.50E-05	0.96	NA	NA
4	rs7667718	154951092	0.50	0.35	2.33	4.87E-05	0.94	NA	NA
4	rs10006749	154951278	0.50	0.35	2.33	4.87E-05	0.94	NA	NA
4	rs1902467	154951578	0.50	0.35	2.33	4.88E-05	0.94	NA	NA
4	rs11723258	154952520	0.50	0.35	2.33	4.90E-05	0.94	NA	NA
4	rs7680824	154953085	0.50	0.36	2.47	3.11E-05	0.89	NA	NA
4	rs1456401	154953422	0.50	0.35	2.33	4.90E-05	0.94	NA	NA
4	rs10031057	154966256	0.50	0.36	2.35	5.21E-05	0.93	NA	NA
4	rs7682762	154978052	0.51	0.37	2.45	4.03E-05	0.89	NA	NA
4	rs7682436	154978117	0.50	0.36	2.38	5.86E-05	0.91	NA	NA
4	rs13139425	154979129	0.50	0.36	2.38	5.92E-05	0.91	NA	NA
4	rs13119833	154980346	0.50	0.36	2.38	5.95E-05	0.91	NA	NA
4	rs13101315	154980735	0.50	0.37	2.40	6.08E-05	0.89	NA	NA
4	rs5018782	154981386	0.50	0.36	2.38	5.96E-05	0.91	NA	NA
4	rs5018783	154981427	0.50	0.36	2.38	5.99E-05	0.91	NA	NA
4	rs5018784	154981437	0.50	0.36	2.38	6.04E-05	0.90	NA	NA
4	rs5018785	154981510	0.49	0.62	0.41	6.51E-05	0.88	NA	NA
4	rs2405206	154982258	0.50	0.36	2.38	6.09E-05	0.90	NA	NA
4	rs1598633	154982287	0.50	0.36	2.38	6.13E-05	0.90	NA	NA
4	rs7680792	154983049	0.50	0.36	2.38	6.14E-05	0.90	NA	NA
4	rs4401438	154984644	0.50	0.36	2.39	6.26E-05	0.90	NA	NA
4	rs4513550	154984743	0.50	0.36	2.39	6.32E-05	0.90	NA	NA
4	rs6823476	154984784	0.50	0.36	2.39	6.33E-05	0.90	NA	NA
4	rs897612	154984867	0.50	0.36	2.39	6.37E-05	0.90	NA	NA
4	rs12509282	154986084	0.50	0.37	2.39	6.44E-05	0.90	NA	NA
5	rs2410936	106501648	0.06	0.15	0.27	8.90E-05	1.00	NA	NA
5	rs13357822	167134292	0.05	0.10	0.17	5.41E-05	0.95	ODZ2	intron
6	rs4946727	106680065	0.21	0.07	0.27	2.88E-05	0.99	NA	NA
6	rs7761791	106683679	0.45	0.25	2.36	1.73E-05	1.00	NA	NA
6	rs6903903	106684200	0.45	0.26	0.41	1.87E-05	0.97	NA	NA
6	rs17514051	119576443	0.29	0.15	2.79	7.78E-05	0.98	MAN1A1	intron
6	rs7770777	119593904	0.29	0.14	2.71	7.40E-05	1.00	MAN1A1	intron
6	rs12198667	119605859	0.29	0.14	0.37	7.39E-05	1.00	MAN1A1	intron
6	rs7753492	119606742	0.29	0.14	0.37	7.39E-05	1.00	MAN1A1	intron
6	rs12192420	119607599	0.29	0.14	0.37	7.18E-05	1.00	MAN1A1	intron
6	rs11751945	119614780	0.29	0.14	0.37	6.75E-05	1.00	MAN1A1	intron

Supplementary Table S2
Continued

Chr	SNP	BP	MAF case	MAF control	OR	*p*	Quality	Gene	SNP type
6	rs7740993	119616700	0.29	0.14	0.36	6.58E-05	1.00	MAN1A1	intron
6	rs11153800	119622517	0.30	0.15	2.80	4.40E-05	0.99	MAN1A1	intron
6	rs12205826	119628503	0.30	0.15	2.75	4.58E-05	0.99	MAN1A1	intron
6	rs11153803	119632568	0.30	0.15	2.70	5.28E-05	0.99	MAN1A1	intron
6	rs11153805	119653359	0.30	0.15	2.70	5.16E-05	0.99	MAN1A1	intron
6	rs1022869	119655780	0.30	0.15	2.70	5.13E-05	0.99	MAN1A1	intron
6	rs7760582	119659056	0.30	0.15	2.70	5.07E-05	0.99	MAN1A1	intron
6	rs6909928	119659906	0.30	0.15	2.71	5.05E-05	0.99	MAN1A1	intron
6	rs7743824	119662926	0.30	0.15	2.71	5.00E-05	0.99	MAN1A1	intron
6	rs10457352	119665757	0.30	0.14	0.37	4.76E-05	0.99	MAN1A1	intron
6	rs11153808	119667753	0.30	0.14	0.37	4.69E-05	0.99	MAN1A1	intron
6	rs10457353	119668056	0.30	0.14	0.36	4.67E-05	0.99	MAN1A1	intron
6	rs11759899	119670815	0.30	0.14	0.36	4.63E-05	0.99	MAN1A1	intron
6	rs6913654	119672875	0.30	0.14	2.75	4.62E-05	0.99	MAN1A1	intron
6	rs10485001	119675324	0.30	0.14	2.75	4.64E-05	0.99	MAN1A1	intron
6	rs7767198	119675888	0.30	0.14	2.75	4.68E-05	0.99	MAN1A1	intron
6	rs12205260	119677438	0.30	0.14	2.75	4.71E-05	0.99	MAN1A1	intron
6	rs10456921	119679026	0.30	0.14	2.74	4.77E-05	0.99	MAN1A1	intron
6	rs11153812	119679931	0.30	0.14	2.74	4.82E-05	0.99	MAN1A1	intron
6	rs11962938	119682759	0.30	0.14	2.74	5.02E-05	0.99	MAN1A1	intron
6	rs10872177	119684399	0.30	0.14	0.37	5.04E-05	0.99	MAN1A1	intron
6	rs6920832	119730755	0.23	0.12	0.28	4.91E-05	0.90	NA	NA
6	rs9489697	119741223	0.38	0.24	0.39	5.66E-05	0.98	NA	NA
6	rs6936790	119749117	0.39	0.24	0.39	5.10E-05	0.99	NA	NA
6	rs6569076	119751989	0.39	0.24	0.39	5.13E-05	0.99	NA	NA
6	rs6904915	119780447	0.39	0.24	2.53	5.62E-05	0.99	NA	NA
6	rs12527248	119789297	0.39	0.24	0.40	5.73E-05	0.99	NA	NA
6	rs2036257	119801100	0.39	0.24	0.40	5.78E-05	0.99	NA	NA
7	rs3887627	57282944	0.35	0.21	2.49	2.73E-05	0.97	NA	NA
7	rs3931139*	138093331	0.37	0.23	2.50	8.28E-05	0.92	ATP6V0A4	intron
7	rs7780678*	138103892	0.40	0.26	2.54	2.11E-05	0.98	ATP6V0A4	intron
8	rs10957176	62069205	0.12	0.20	0.25	6.60E-05	0.86	NA	NA
8	rs1525053	69296139	0.18	0.08	0.22	5.61E-05	0.91	DEPDC2	intron
8	rs7463918	113473777	0.17	0.30	0.34	5.83E-05	0.93	CSMD3	intron
9	rs1006116	110381485	0.32	0.46	0.42	8.26E-05	0.99	NA	NA
9	rs10982662	117104713	0.21	0.29	0.30	8.33E-05	0.82	1-Dec	intron
9	rs10982663	117106399	0.21	0.29	0.30	8.34E-05	0.82	1-Dec	intron
9	rs10983328	118530159	0.18	0.32	0.32	6.72E-05	0.86	ASTN2	intron
9	rs7028544	118530393	0.26	0.44	0.39	6.63E-05	1.00	ASTN2	intron
10	rs17101073	84669660	0.11	0.03	0.20	8.36E-05	0.98	NRG3	intron
10	rs11814517	84681945	0.11	0.03	0.22	5.67E-05	1.00	NRG3	intron
10	rs17101125	84683470	0.11	0.03	4.56	5.45E-05	1.00	NRG3	intron
10	rs10509462	84688185	0.11	0.03	0.22	4.35E-05	1.00	NRG3	intron
10	rs17101130	84688446	0.11	0.03	4.61	4.31E-05	1.00	NRG3	intron
10	rs7069185	84706503	0.11	0.03	0.21	2.31E-05	1.00	NRG3	intron
10	rs17101139	84708657	0.11	0.03	0.21	2.28E-05	1.00	NRG3	intron
10	rs11815363	84712638	0.11	0.03	4.79	2.25E-05	1.00	NRG3	intron
10	rs11816685	84712859	0.11	0.03	4.79	2.23E-05	1.00	NRG3	intron
10	rs11819041	84724809	0.12	0.03	4.84	1.85E-05	1.00	NRG3	intron
10	rs17101164	84727384	0.12	0.03	0.21	1.70E-05	1.00	NRG3	intron
10	rs999799	84728972	0.12	0.03	4.83	1.61E-05	1.00	NRG3	intron
10	rs17101193	84734906	0.12	0.03	4.83	1.62E-05	1.00	NRG3	missense
10	rs17101196	84735020	0.12	0.03	0.21	1.62E-05	1.00	NRG3	synonymous
10	rs7909420	84741572	0.12	0.03	0.21	1.63E-05	1.00	NA	NA
10	rs17101209	84745160	0.12	0.03	0.21	1.63E-05	1.00	NA	NA
10	rs17101227	84757598	0.12	0.03	0.22	1.80E-05	0.99	NA	NA
10	rs12570609	129058140	0.45	0.31	2.46	1.75E-05	0.93	DOCK1	intron
10	rs7914006	129059422	0.44	0.31	2.42	2.44E-05	0.93	DOCK1	intron
11	rs10832683	16790037	0.29	0.20	3.92	6.55E-05	0.73	PLEKHA7	intron
11	rs7103236	42018659	0.05	0.08	0.16	7.59E-05	0.95	NA	NA
12	rs736107	12518677	0.06	0.02	47.83	3.37E-06	0.94	NA	NA

Supplementary Table S2
Continued

Chr	SNP	BP	MAF case	MAF control	OR	*p*	Quality	Gene	SNP type
12	rs2287539	14585501	0.15	0.26	0.36	6.66E-05	1.00	FLJ22662	intron
12	rs1862013	14586144	0.15	0.26	0.37	6.68E-05	1.00	FLJ22662	intron
12	rs7296684	14598395	0.15	0.26	0.36	6.40E-05	0.99	FLJ22662	intron
12	rs2032762	14599040	0.15	0.26	0.36	6.30E-05	0.99	FLJ22662	intron
12	rs12424762	36929753	0.06	0.01	0.03	5.27E-05	0.97	NA	NA
12	rs12425010	36970274	0.06	0.01	0.03	4.17E-05	0.97	NA	NA
12	rs12422226	37042040	0.06	0.01	0.03	3.50E-05	0.97	NA	NA
12	rs7310514	37053411	0.06	0.01	27.77	3.39E-05	0.97	NA	NA
12	rs12423659	37265907	0.07	0.01	0.05	2.60E-05	0.98	NA	NA
12	rs1021257	37425785	0.08	0.02	0.06	9.49E-06	0.98	CPNE8	intron
12	rs12230422	37447314	0.12	0.04	0.19	8.84E-05	0.98	CPNE8	intron
12	rs10876062	37454453	0.18	0.07	4.28	4.23E-05	0.98	CPNE8	intron
12	rs826837	37470792	0.19	0.09	0.26	6.01E-05	0.98	CPNE8	intron
12	rs826836	37471673	0.19	0.09	3.82	5.96E-05	0.98	CPNE8	intron
12	rs7309194	37494213	0.19	0.08	3.87	5.05E-05	0.98	CPNE8	intron
12	rs12424244	37501919	0.19	0.08	0.25	3.47E-05	0.99	CPNE8	intron
12	rs17126713	37505285	0.19	0.08	3.94	3.32E-05	0.99	CPNE8	intron
12	rs9943730	37529460	0.19	0.08	0.25	3.01E-05	0.98	CPNE8	intron
12	rs12425783	37536951	0.19	0.08	4.04	2.88E-05	0.98	CPNE8	intron
12	rs12422883	37543217	0.19	0.08	4.03	2.93E-05	0.98	CPNE8	intron
12	rs10876185	37544916	0.19	0.08	0.25	2.90E-05	0.98	CPNE8	intron
12	rs11169878	37551227	0.20	0.09	3.37	7.86E-05	1.00	CPNE8	intron
12	rs7311812	37568585	0.08	0.02	0.09	6.35E-05	0.98	CPNE8	intron
12	rs7308580	37571225	0.15	0.05	0.18	1.42E-05	0.99	CPNE8	intron
12	rs7307936	37571373	0.15	0.05	5.60	1.42E-05	0.99	CPNE8	intron
12	rs1516555	37583295	0.15	0.05	5.55	1.45E-05	0.99	CPNE8	intron
12	rs12423647	37593034	0.14	0.05	5.17	2.16E-05	1.00	NA	NA
12	rs1878224	37595981	0.14	0.05	5.12	2.34E-05	1.00	NA	NA
12	rs7968397	37596858	0.14	0.05	0.21	3.70E-05	0.99	NA	NA
12	rs7971601	37596918	0.14	0.05	4.73	3.77E-05	0.99	NA	NA
12	rs7974510	37596997	0.14	0.05	4.72	3.83E-05	0.99	NA	NA
12	rs1878223	37599402	0.14	0.05	0.22	4.30E-05	0.99	NA	NA
12	rs7298320	37604104	0.14	0.06	0.23	6.67E-05	0.98	NA	NA
12	rs12424948	37605219	0.14	0.05	0.22	4.68E-05	0.99	NA	NA
12	rs7294592	74751512	0.20	0.31	0.32	5.73E-05	0.82	NAP1L1	intron
12	rs11180823	74764208	0.23	0.33	0.31	5.42E-05	0.79	NAP1L1	intron
12	rs12297524	127302475	0.36	0.19	0.40	6.16E-05	0.96	NA	NA
12	rs11059603	127302970	0.36	0.19	2.51	6.04E-05	0.96	TMEM132C	promoter
12	rs12299465*	127303503	0.34	0.19	0.37	7.50E-05	0.90	TMEM132C	promoter
12	rs11609257*	127303699	0.36	0.19	0.40	5.74E-05	0.96	TMEM132C	promoter
12	rs12825406	127304152	0.36	0.19	2.52	5.68E-05	0.96	TMEM132C	promoter
12	rs1514898	127304208	0.36	0.19	2.53	5.62E-05	0.96	TMEM132C	promoter
12	rs1193373	127311708	0.25	0.40	0.44	2.86E-05	1.00	TMEM132C	promoter
12	rs1193376*	127312068	0.25	0.40	0.44	2.86E-05	0.99	NA	NA
13	rs9603150	36693584	0.24	0.13	0.33	5.17E-05	0.97	NA	NA
13	rs9315475	36696434	0.24	0.13	3.05	5.02E-05	0.97	NA	NA
13	rs10219784	36710511	0.23	0.12	0.35	7.30E-05	0.99	NA	NA
13	rs1980733	36714086	0.23	0.13	0.35	7.88E-05	0.99	NA	NA
13	rs1980732	36714223	0.23	0.12	2.89	7.46E-05	0.99	NA	NA
13	rs1324020	36720869	0.23	0.13	0.35	7.48E-05	0.99	NA	NA
13	rs9532392	38998591	0.14	0.05	0.24	8.86E-05	0.99	LHFP	intron
14	rs10142046	72117717	0.17	0.09	4.05	8.33E-05	0.91	NA	NA
14	rs11625679*	72118095	0.17	0.09	0.25	7.60E-05	0.92	NA	NA
14	rs12587303	72128367	0.19	0.09	3.57	4.44E-05	0.95	NA	NA
14	rs17780651	72131479	0.14	0.06	0.14	3.23E-06	0.91	NA	NA
14	rs2042045	76837731	0.28	0.14	2.71	8.98E-05	0.96	POMT2	intron
14	rs3815626	76840587	0.29	0.15	0.36	5.05E-05	0.93	POMT2	intron
14	rs2363641	76852887	0.29	0.15	0.36	5.00E-05	0.93	POMT2	intron
14	rs2111699	76858350	0.28	0.15	0.36	5.28E-05	0.93	GSTZ1	intron
14	rs2363643	76858661	0.29	0.15	2.70	5.60E-05	0.94	GSTZ1	5′ UTR
14	rs4147578	76860169	0.22	0.10	3.08	5.34E-05	0.96	GSTZ1	intron

Supplementary Table S2
Continued

Chr	SNP	BP	MAF case	MAF control	OR	*p*	Quality	Gene	SNP type
14	rs8016187	76860625	0.22	0.10	3.01	4.72E-05	0.97	GSTZ1	intron
14	rs2287395	76861272	0.22	0.10	0.35	5.49E-05	1.00	GSTZ1	intron
14	rs2270423	76865391	0.22	0.10	2.86	5.53E-05	1.00	GSTZ1	intron
17	rs2750012*	631011	0.14	0.07	0.18	7.25E-05	0.92	GLOD4	intron
17	rs11658079	639270	0.15	0.07	5.36	4.93E-05	0.91	RNMTL1	intron
17	rs9915388	644926	0.13	0.07	9.46	4.47E-05	0.86	NA	NA
17	rs7215435	645414	0.14	0.09	0.09	3.43E-05	0.83	NA	NA
17	rs16951470	15263319	0.12	0.08	15.46	3.93E-05	0.85	NA	NA
19	rs1368445	35601575	0.08	0.03	0.08	3.04E-05	0.93	ZNF536	intron
19	rs11084710	38344196	0.48	0.30	2.43	1.85E-05	0.98	WDR88	intron
19	rs10407579	38345252	0.48	0.30	0.41	1.89E-05	0.98	WDR88	intron
20	rs2300186	1082900	0.33	0.48	0.41	1.76E-05	0.92	PSMF1	intron
20	rs2300185	1083413	0.34	0.49	0.42	2.27E-05	0.94	PSMF1	intron
20	rs6074191	1084156	0.31	0.47	0.41	1.73E-05	0.91	PSMF1	intron
20	rs4813945	1084656	0.34	0.49	0.42	2.27E-05	0.95	PSMF1	intron
20	rs6134051	1085204	0.34	0.50	0.43	2.28E-05	0.97	PSMF1	intron
20	rs2072965	1094136	0.30	0.46	0.41	1.17E-05	0.92	PSMF1	3′ UTR
20	rs4813044	1096783	0.34	0.50	0.44	1.92E-05	0.98	PSMF1	3′
20	rs3746814	1100237	0.33	0.49	0.43	2.07E-05	0.95	NA	NA
20	rs6040293	1101225	0.30	0.46	0.42	2.18E-05	0.91	NA	NA
20	rs7273511	8446416	0.25	0.37	0.33	8.01E-05	0.88	PLCB1	intron
22	rs2187898	25676779	0.36	0.20	0.40	6.89E-05	0.99	NA	NA
22	rs5761859	25677402	0.36	0.20	0.40	6.89E-05	0.99	NA	NA
22	rs5761860	25677493	0.36	0.20	2.49	6.89E-05	0.99	NA	NA
22	rs5752451	25678321	0.36	0.20	2.49	6.91E-05	0.99	NA	NA
22	rs5761863	25678456	0.36	0.20	2.49	6.86E-05	0.99	NA	NA

*SNP was nominally associated with AD in the meta-analysis, OR = odds ratio, Quality = the posterior probability of a correctly imputed genotype.